0590
09/13 #5

OIPE

RAW SEQUENCE LISTING DATE: 09/16/2002
PATENT APPLICATION: US/10/005,438 TIME: 15:21:40

Input Set : N:\Crf3\RULE60\10005438.raw
Output Set: N:\CRF4\09162002\J005438.raw


```
 1 <110> APPLICANT: Tse Wen Chang
 2       Liming Yu
 3 <120> TITLE OF INVENTION: Hybrid with Interferon-alpha and an
 4       Immunoglobulin Fc for Treatment of Tumors
 5 <130> FILE REFERENCE: 95-2AAA
 7 <140> CURRENT APPLICATION NUMBER: 10/005,438
 8 <141> CURRENT FILING DATE: 2001-12-03
10 <150> PRIOR APPLICATION NUMBER: US/09/268,787
11 <151> PRIOR FILING DATE: 1999-03-16
14 <150> PRIOR APPLICATION NUMBER: 08/994,719
15 <151> PRIOR FILING DATE: 1997-12-19
16 <150> PRIOR APPLICATION NUMBER: 08/719,331
17 <151> PRIOR FILING DATE: 1996-09-25
18 <150> PRIOR APPLICATION NUMBER: 08/579,211
19 <151> PRIOR FILING DATE: 1995-12-28
20 <160> NUMBER OF SEQ ID NOS: 11
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1254
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)...(1251)
30 <223> OTHER INFORMATION: recombinant sequence based on human sequences
31 <400> SEQUENCE: 1
32       atg gcc ttg acc ttt gct tta ctg gtg gcc ctc ctg gtg ctc agc tgc       48
33       Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
34        1               5                  10                  15
35       aag tca agc tgc tct ctg ggc tgt gat ctg cct caa acc cac agc ctg       96
36       Lys Ser Ser Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Ser Leu
37                   20                  25                  30
38       ggt agc agg agg acc ttg atg ctc ctg gca cag atg agg aaa atc tct      144
39       Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Lys Ile Ser
40                35                  40                  45
41       ctt ttc tcc tgc ttg aag gac aga cat gac ttt gga ttt ccc cag gag      192
42       Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
43            50                  55                  60
44       gag ttt ggc aac cag ttc caa aag gct gaa acc atc cct gtc ctc cat      240
45       Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
46        65                  70                  75                  80
47       gag atg atc cag cag atc ttc aat ctc ttc agc aca aag gac tca tct      288
48       Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
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                    85                  90                  95
gct gct tgg gat gag acc ctc cta gac aaa ttc tac act gaa ctc tac      336
Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
            100                 105                 110
cag cag ctg aat gac ctg gaa gcc tgt gtg ata cag ggg gtg ggg gtg      384
Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
        115                 120                 125
aca gag act ccc ctg atg aag gag gac tcc att ctg gct gtg agg aaa      432
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
    130                 135                 140
tac ttc caa aga atc act ctc tat ctg aaa gag aag aaa tac agc cct      480
Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
145                 150                 155                 160
tgt gcc tgg gag gtt gtc aga gca gaa atc atg aga tct ttt tct ttg      528
Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
                165                 170                 175
tca aca aac ttg caa gaa agt tta aga agt aag gaa gag tcc aaa tat      576
Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu Glu Ser Lys Tyr
            180                 185                 190
ggt ccc ccg tgc cca tca tgc cca gca cct gag ttc ctg ggg gga cca      624
Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
        195                 200                 205
tca gtc ttc ctg ttc ccc cca aaa ccc aag gac act ctc atg atc tcc      672
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
    210                 215                 220
cgg acc cct gag gtc acg tgc gtg gtg gtg gac gtg agc cag gaa gac      720
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
225                 230                 235                 240
ccc gag gtc cag ttc aac tgg tac gtg gat ggc gtg gag gtg cat aat      768
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                245                 250                 255
gcc aag aca aag ccg cgg gag gag cag ttc aac agc acg tac cgt gtg      816
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
            260                 265                 270
gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aac ggc aag gag      864
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
        275                 280                 285
tac aag tgc aag gtc tcc aac aaa ggc ctc ccg tcc tcc atc gag aaa      912
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
    290                 295                 300
acc atc tcc aaa gcc aaa ggg cag ccc cga gag cca cag gtg tac acc      960
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
305                 310                 315                 320
ctg ccc cca tcc cag gag gag atg acc aag aac cag gtc agc ctg acc     1008
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
                325                 330                 335
tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag     1056
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            340                 345                 350
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Input Set : N:\Crf3\RULE60\10005438.raw
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```
98        agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg     1104
99        Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
100                355                 360                 365
101        gac tcc gac ggc tcc ttc ttc ctc tac agc agg ctg acc gtg gac aag     1152
102        Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
103            370                 375                 380
104        agc agg tgg cag gag ggg aat gtc ttc tca tgc tcc gtg atg cat gag     1200
105        Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
106        385                 390                 395                 400
107        gct ctg cac aac cac tac aca cag aag agc ctc tcc ctg tct ctg ggt     1248
108        Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
109                        405                 410                 415
110        aaa tag                                                         1254
111        Lys
113 <210> SEQ ID NO: 2
114 <211> LENGTH: 417
115 <212> TYPE: PRT
116 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: artificial peptide sequence based on human
119       sequence
120 <400> SEQUENCE: 2
121       Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
122        1               5                  10                  15
123       Lys Ser Ser Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Ser Leu
124                   20                  25                  30
125       Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Lys Ile Ser
126               35                  40                  45
127       Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
128           50                  55                  60
129       Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
130       65                  70                  75                  80
131       Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
132                       85                  90                  95
133       Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
134                   100                 105                 110
135       Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
136               115                 120                 125
137       Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
138           130                 135                 140
139       Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
140       145                 150                 155                 160
141       Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
142                       165                 170                 175
143       Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu Glu Ser Lys Tyr
144                   180                 185                 190
145       Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
146               195                 200                 205
147       Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
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```
148          210                 215                 220
149      Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
150      225                 230                 235                 240
151      Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
152                      245                 250                 255
153      Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
154                  260                 265                 270
155      Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
156              275                 280                 285
157      Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
158          290                 295                 300
159      Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
160      305                 310                 315                 320
161      Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
162                      325                 330                 335
163      Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
164                  340                 345                 350
165      Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
166              355                 360                 365
167      Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
168          370                 375                 380
169      Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
170      385                 390                 395                 400
171      Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
172                      405                 410                 415
173      Lys
175 <210> SEQ ID NO: 3
176 <211> LENGTH: 2
177 <212> TYPE: PRT
178 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: artificial peptide linker sequence
181 <400> SEQUENCE: 3
182      Gly Ser
183       1
185 <210> SEQ ID NO: 4
186 <211> LENGTH: 7
187 <212> TYPE: PRT
188 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: artificial peptide linker sequence
191 <400> SEQUENCE: 4
192      Gly Gly Ser Gly Gly Gly Ser
193       1               5
195 <210> SEQ ID NO: 5
196 <211> LENGTH: 12
197 <212> TYPE: PRT
198 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
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Input Set : N:\Crf3\RULE60\10005438.raw
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<223> OTHER INFORMATION: artificial peptide linker sequence
<400> SEQUENCE: 5
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10
<210> SEQ ID NO: 6
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: artificial peptide linker sequence
<400> SEQUENCE: 6
Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15
Ser
<210> SEQ ID NO: 7
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: artificial peptide linker sequence
<400> SEQUENCE: 7
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
1 5 10 15
Gly Ser Gly Gly Gly Gly Ser
20
<210> SEQ ID NO: 8
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: artificial peptide linker sequence
<400> SEQUENCE: 8
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly
1 5 10 15
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30
<210> SEQ ID NO: 9
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: artificial peptide linker sequence
<400> SEQUENCE: 9
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly
1 5 10 15
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30
Gly Gly Ser Gly Gly Gly Gly Ser
35 40

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/005,438

DATE: 09/16/2002
TIME: 15:21:41

Input Set : N:\Crf3\RULE60\10005438.raw
Output Set: N:\CRF4\09162002\J005438.raw